

B1  
conclusion  
containing all possible base sequences of that predetermined length and the  
base sequences being incapable of ligating to each other; and  
(b) a means for resolving a measured quantity of a hybridized probe into  
quantities which correspond to unique amounts of the templates to which the  
probe hybridizes.

B2  
36. (Amended) A kit according to claim 33, wherein the base sequence of each  
probe is unphosphorylated at both [31] 3' and [51] 5' ends.

Kindly add new claims 41-43.

B3  
A41. A method of using the kit of claim 33 comprising:  
(a) contacting a target DNA population with the array of hybridization  
probes;  
(b) cleaving the labels from hybridized probes to identify the hybridized  
probes; and  
(c) determining the sequence of the DNA from the identity of the  
hybridized probes.

42. A kit according to claim 33, wherein the means comprises an algorithm.

43. A kit according to claim 33, wherein the means comprises a computer  
program.